

FIGURE 1

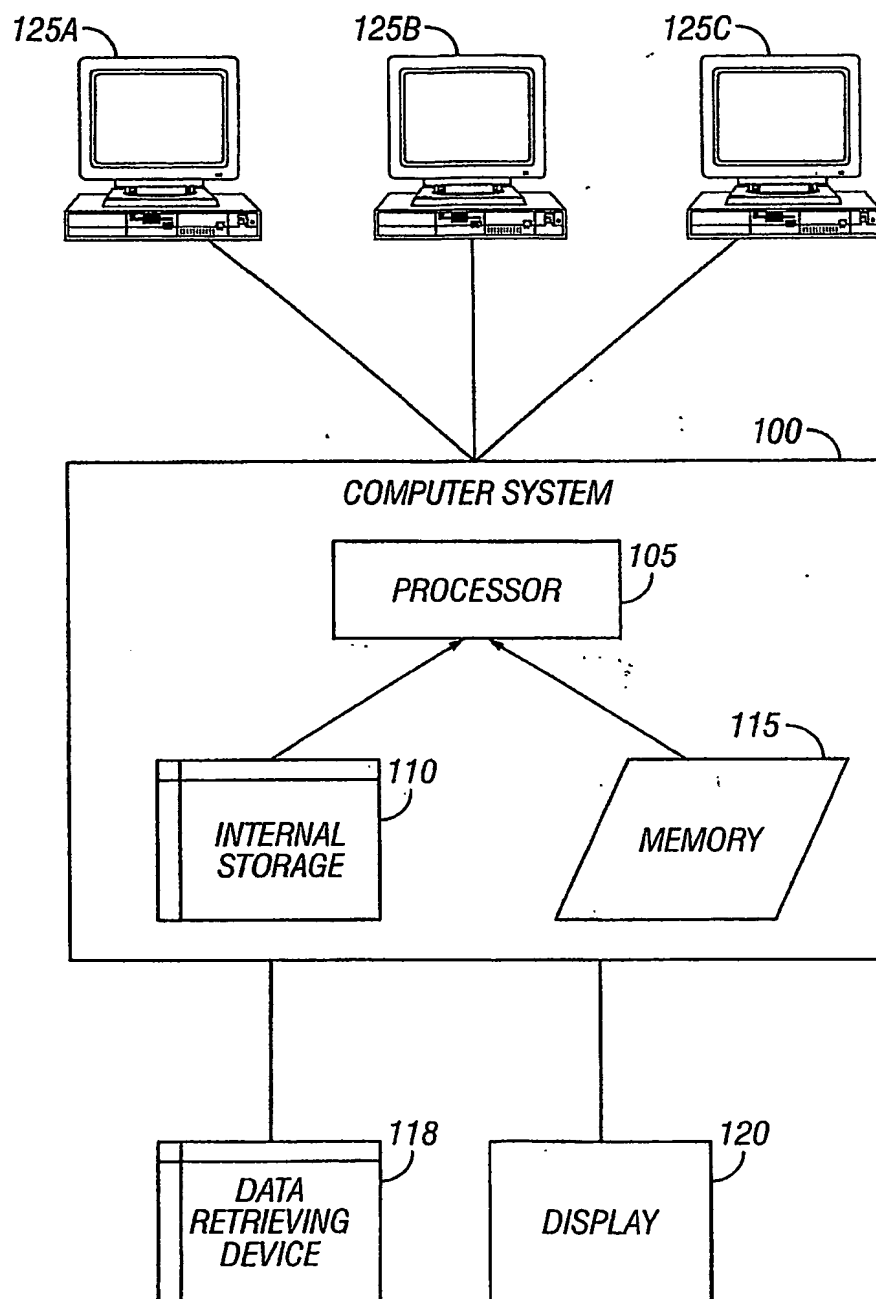


FIGURE 2

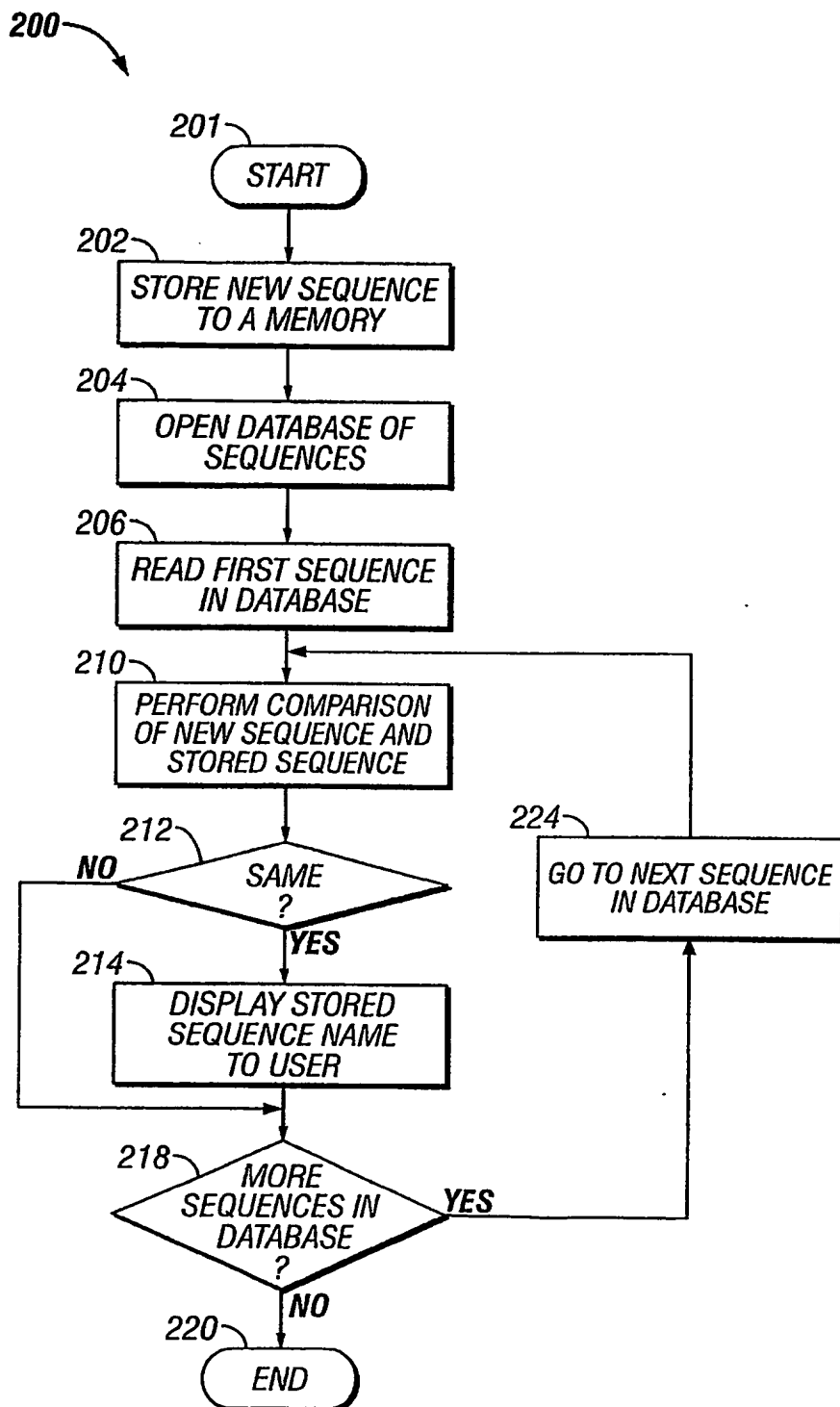


FIGURE 3

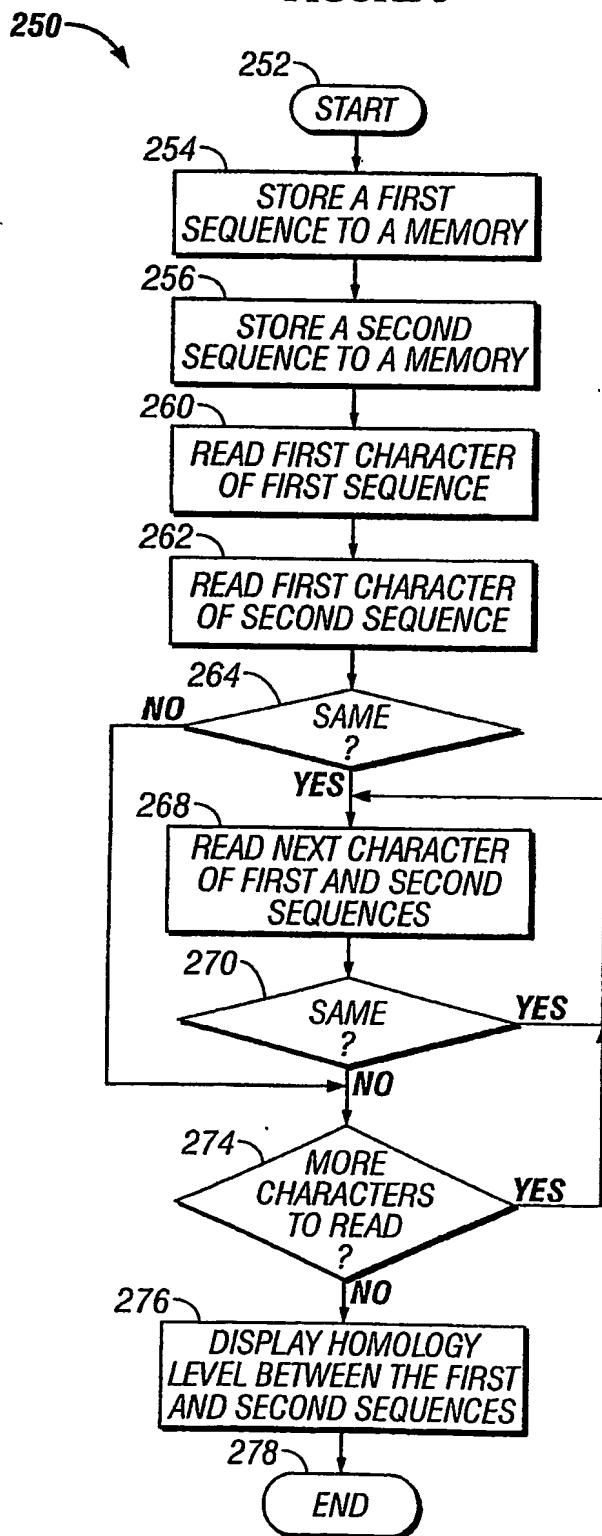


FIGURE 4

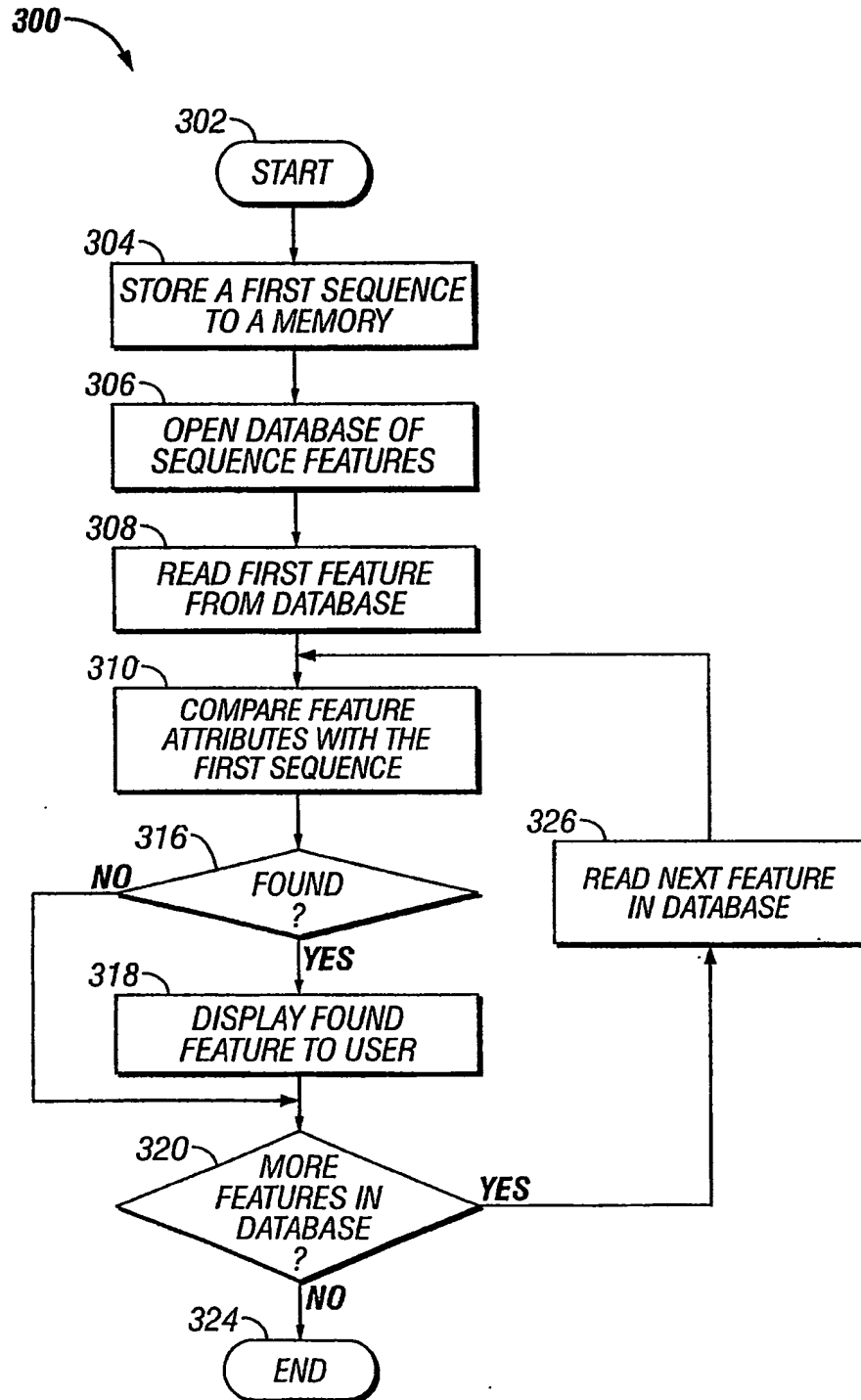


FIGURE 5

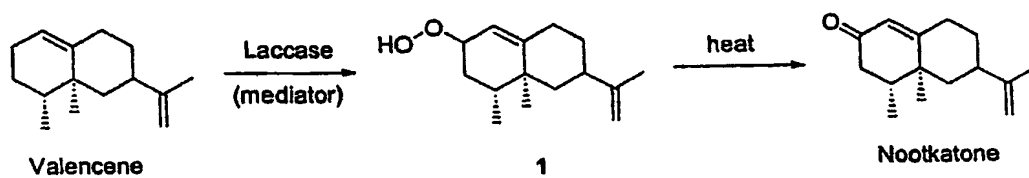


FIGURE 6

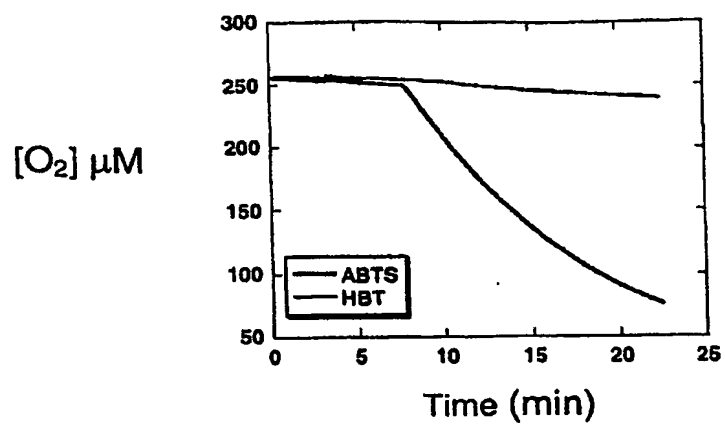


FIGURE 7

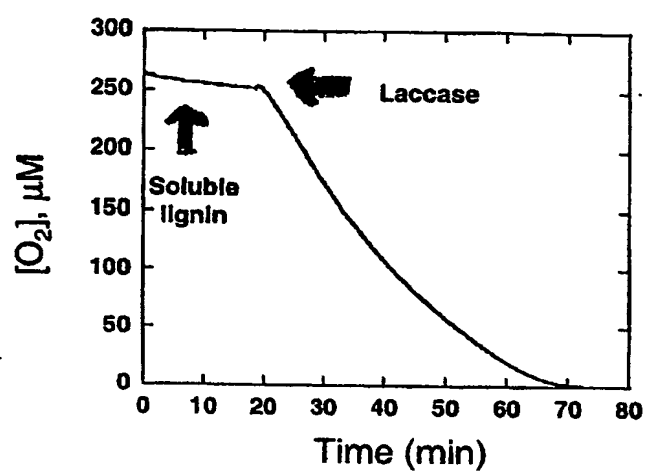


FIGURE 8

Enzyme, 57 mU	ABTS	HBT			TEMPO	Lignin, pH 9 (4 mg/ml)
		pH 5	pH 7	pH 9		
<i>T. versicolor</i>	16.5	0.52	0.08	0 <sup>2</sup>	0 <sup>2</sup>	-
<i>P. ostreatus</i>	19	-	-	0.8 <sup>2</sup>	3.0 <sup>2</sup>	7.45 <sup>2</sup>
SEQ ID NOS:15, 16 (expressed in <i>Pichia</i> )	17.4	0.15	0	0	0.8 <sup>2</sup>	6.2 ± 2.4
SEQ ID NOS:15, 16 <sup>1</sup>	15	TBD	0.32	0.57	12.6 <sup>2</sup>	20 ± 0.35
SEQ ID NOS:9, 10 <sup>1</sup>	14.2	TBD	TBD	TBD	TBD	
SEQ ID NOS:5, 6 <sup>1</sup>	3.6	0.37	0.1	0.1	0.31 <sup>2</sup>	0
SEQ ID NOS:13, 14 <sup>1</sup> (expressed in <i>Pichia</i> )	8 <sup>3</sup>	0	0.06	0	TBD	6
SEQ ID NOS:13, 14 <sup>1</sup>	10.8 <sup>3</sup>	0.16 <sup>3</sup>	0.29	0.3	1.4 <sup>2</sup>	1.8
SEQ ID NOS:19, 20	5.7	0		0.08		

<sup>1</sup>includes 100  $\mu$ M CuSO<sub>4</sub>; <sup>2</sup>0.3 U enzyme; <sup>3</sup>pH 6



FIGURE 9

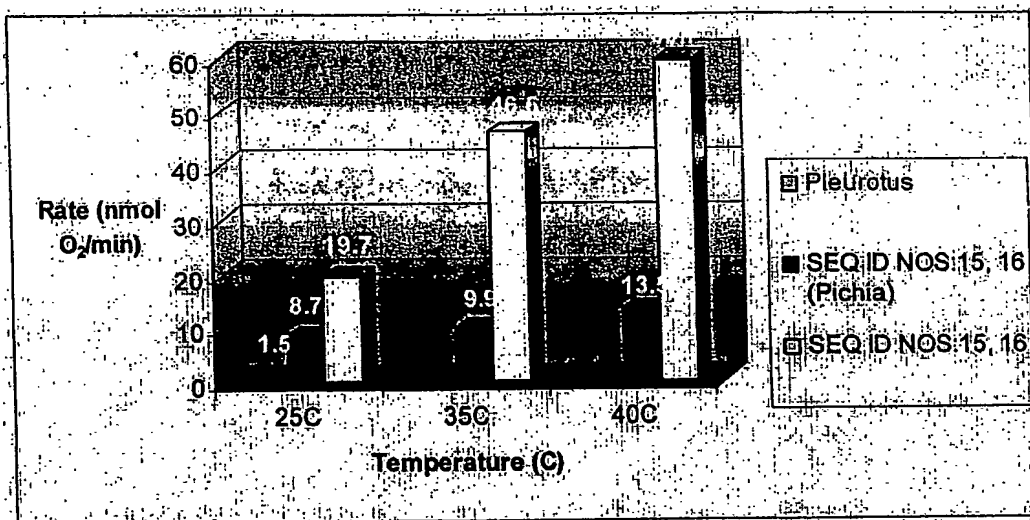


FIGURE 10

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      10      20      30      40      50      60
SEQ ID NO:4 MLRPEDATRRRAFIHAATMSCLVAAGASGLTLTREVRAGFRAPNPFQFIPDLEIQLNAREDH 60
SEQ ID NO:8 -MDGFVESRRREFIRTTGWT-----AGAMLFSSQNLEFAAAABAAADYT-----VRIKA--AP 48
Consensus   :   ** **:: * :   .. *:: : : * \ * : :   : : : * 27

      70      80      90      100     110     120
SEQ ID NO:4 VSILPGPLTRVWRVDGKVVKGDPGNLAFLSNGYLEVVRVRRCOKVRIQFVNQLAEFTIIF 120
SEQ ID NO:8 IETASDKILSTITYNGQFPG-----PLIRLKEGROVTVDIENETDTEQILH 94
Consensus   : : * .. : : * : : :   * : : : : : : * : : : * : * 52

      130     140     150     160     170     180
SEQ ID NO:4 WHGLYVPAAMDGHPRN-----AVSTGEHYVYEFETIANQAGTYWFFHAHPDGRRTGAQIYFGLA 176
SEQ ID NO:8 WHGQFVSPDVGAAEEGTPIYPAHQRRIMFTPGPAGLRFYHTENRAGADLSLGOYSGOV 154
Consensus   *** : : : : * : : :   : * : :   * * : : : : * * . 71

      190     200     210     220     230     240
SEQ ID NO:4 CVLIVDDEFAAAGLPFGPYDVPLVIQDRITFDDRNQFTYLAEGNEGMMGGMMGNGGMMGRG 236
SEQ ID NO:8 GPVYIEPKENPCRYDREVFLVLKEFEP--ILSRGGDMEQDFLSPSAIDKTLKETCEAAMKA 213
Consensus   * : : : * .. : : * : : : : : : : : : : : * : : : 89

      250     260     270     280     290     300
SEQ ID NO:4 GMMGGGGMGOMMARMMGFLGDRILVNGKEEDFVLPVAARAYRLRLNGSNTRIYKLAWSDR 296
SEQ ID NO:8 SLAKRMPHGGEYVGYKFTTINGRMIGHGE--IRVKHGERVLFHILNGSATETIRSLALPDH 271
Consensus   : :   * : : : : : : * : : * : : : : : : : : : : : : 115

      310     320     330     340     350     360
SEQ ID NO:4 TPLTVICTDGGLLERPVTRQYVTLAPAERVDVWVDFSRWPGTKLTLOS-LAFDGVLAG 355
SEQ ID NO:8 S-FEVIALDGNPVPNPVHVPVLWLGTAERTSAVVEMNHPGVWILGDLADDDRNHGMGVV 330
Consensus   : : ** . ** : : ** : : * . : : : : * : : : : : : : 139

      370     380     390     400     410     420
SEQ ID NO:4 GMIGNTSLESGASEFVLKVGVVDQRANTKMBLEARLASLPPVRFQDAVNAHNPKVENITMG 415
SEQ ID NO:8 EYACRSCKPHWATFPFRWDYARFAKPNASAE-----EADAEADMTFAKDNAAEAG 381
Consensus   * : : * * : : * : : : : : : : : : : : : : : * 158

      430     440     450     460     470     480
SEQ ID NO:4 MMVVGVNCRRFEMNCVAKTETVRRNSTEIWEEFNESMMLMAHSMVHGLOFRVLERTVQ 475
SEQ ID NO:8 FNRRTINGVAYPMSNEMAPASFHLRQGKRYILMRN-ASDDIIFIELRHSEFLAN---- 436
Consensus   : * : ** : * : : : : : : : : : : : : : : : : : : 180

      490     500     510     520     530     540
SEQ ID NO:4 PDFRAGYRTLAAGLVDDGKWDIVLLMFCERIRLLLRFASTGLFLYHCFMLEHEDSGLMR 535
SEQ ID NO:8 -----LACTKTACVMKDVVMLGGYQOLEIDFVADNPGLTFLFCHQOLEMDRCFMA 486
Consensus   : : : * : : : : : : : : : : : : : : : : : : : 203

      . . . . |
SEQ ID NO:4 NYLIQT 541
SEQ ID NO:8 LFDYV- 491
Consensus   : 204

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	10	20	30	40	50	60
SEQ ID NO:2	MTREKFVDALPIPD	TLKPVQSKDSTY	YEVTMEECYHQLHR			D 42
SEQ ID NO:16	MTLEKFVDALPIPD	TLKPVQSKDSTY	YEVTMEECYHQLHR			D 42
SEQ ID NO:18		MDVGGPVD	Y-YEIAVRQFQQQILPP			P 25
SEQ ID NO:20	MTTRRDFLKRAGLGLAA	ATLPVLSCGPCDALFRYGV	ATRRSADGLDTRLRLRFSHTCIG			60
SEQ ID NO:26		MATVPATTRFPAALG	TGRDSP			21
SEQ ID NO:14	MTAAGAALTASGLLISRTSLSD	TRAGGPAGASPF	AAQPVAAQALAP			IV 48
SEQ ID NO:6	MDRRKFIKTSLSF	SALGFVSGGLSLSCGGGGGTGSSSGQGS				42
Consensus						1
	70	80	90	100	110	120
SEQ ID NO:2	LPPTRLWGYN	LFPGP	TIKAKRNENVYVKWMNNLPS			EHFLPIDHTI 88
SEQ ID NO:16	LPPTRLWGYN	LFPGP	TIKAKRNENVYVKWMNNLPS			EHFLPIDHTI 88
SEQ ID NO:18	LPATTVWSYGSTNHSGTF	NYPAFTIEAKWNT	PVRVKWINDLKDLS	SGEFLPHLLPVDPTL		85
SEQ ID NO:20	HEQVYTRAYDG	RIPGPVLRVKPGDTL	KIRLINDLPDE			E---DGH 101
SEQ ID NO:26				VISGLAD		28
SEQ ID NO:14	TPFRTAMPIPP	VARPVSVTSTTD	TSYIPVTQTAEIIPG			VRTPVL 93
SEQ ID NO:6	TLKQSLNIPG	YFLFPDQQRVSITAKWTT	LEVIPGKST			DMLVYEIDN 89
Consensus						1
	130	140	150	160	170	180
SEQ ID NO:2	HHSDS	QHA	EPVKT	VVHL	GGVTPDDSDGY	PEAWFS 124
SEQ ID NO:16	HHSDS	QHA	EPVKT	VVHL	GGVTPDDSDGY	PEAWFS 124
SEQ ID NO:18	HWANPPGGLGGRDMR	PEFTTTPDPYRGPVPIVTHL	GGTSQES	DGFTEAWYLPTATNIP		145
SEQ ID NO:20	GHA	KS	DDVNVPHGFN	TTNIT	THGLHVSPGNSDNV	VF 138
SEQ ID NO:26				VTNLT	THGFHVSPGNSDNIFL	50
SEQ ID NO:14	TYGGSFPGPTIKARSGRRV	VVKQPNRITTGTSMHL	GAVVDPANDG	GEMDLIT		146
SEQ ID NO:6	EYNPVI	FLRKGQTSAD	EVNNSGED	SIH	HWGFRAPWKS	DGHYYAVK 137
Consensus						3
	190	200	210	220	230	240
SEQ ID NO:2	KDFEQTGPYFK		RE	VYHYENQ	ORGAILWYHD	HAMALTRLNVYAG 167
SEQ ID NO:16	KDFEQTGPYFK		RE	VYHYENQ	ORGAILWYHD	HAMALTRLNVYAG 167
SEQ ID NO:18	AGFATEGTWDYTFKTQ	FLNQGVFWQPGSAIFQYAND	ORASTLWYHD	HALGMTRLNVYAG		205
SEQ ID NO:20	Q	IPP	GTHFD	YE	YNIDANHPAGTFF	YHPHKGHSVTNQMMG 178
SEQ ID NO:26	H	INPGETFD		YE	FKLPANHSFGMYWYH	PHGHGDTAPQCNG 90
SEQ ID NO:14		PGGORT		Y	TENQVAATLWYHD	HAHMEAEHVYRG 181
SEQ ID NO:6		DGETYS		Y	PDFTIIDRS	GYFYHPPHGRTGYQVYYG 173
Consensus						10
	250	260	270	280	290	300
SEQ ID NO:2	LICAYIIHEPKE		KRLKLP	SGE	YDVPL	LITDRTINEDGSLFYPSG 211
SEQ ID NO:16	LICAYIIHEPKE		KRLKLP	SGE	YDVPL	LITDRTINEDGSLFYPSG 211
SEQ ID NO:18	PAGFYLLRGGPDDMV	VGTLPGPAPALDD	PSGMKY	YDIPLAIQDRSF	NKDSLFYPSDSR	263
SEQ ID NO:20	MAGALIVEGDID		RV	PEIAAA	KDYIFLLQELRFEED	GHAPA 218
SEQ ID NO:26	MAGVILIDGGLD		EV	GIAGL	TERLLVLQATQFDG	GN 127
SEQ ID NO:14	MSGFYLI	SDNE	DALPL	RG	T	YDVPIVRDIGNPDGTLFFDHN 225
SEQ ID NO:6	LAMIIIEDEDE		DNLKQALD	LEYGVIDIPLI	IQDKTFDSS	QOLVYN 219
Consensus						20
	310	320	330	340	350	360
SEQ ID NO:2	PENPSPSLPN	PSIVPAFCGDTIL	VNGKAWPYMEVEP	RKYRFR	RVINASNTRTY	263
SEQ ID NO:16	PENPSPSLPN	PSIVPAFCGDTIL	VNGKAWPYMEVEP	RKYRFR	RVINASNTRTY	263
SEQ ID NO:18	RFFDGFKKAYIPDS	DISPIWNPEFFGKVMV	VNNGR	SWPFL	EV	EP

FIGURE 11B

SEQ ID NO:20	----HFPFHDLN-----LMLFR--TVNGQVNP	TIYLRPGEVQRWRFIHAGVEHYL	263
SEQ ID NO:26	----LVPYNNQSN-----ATRQR--FVNGQLNP	TIYLRPGEVQRWRFIHAGVEHYL	172
SEQ ID NO:14	-----FDTRPQ-----ILVNGKPO	PIYFQVAA-RKYRLRLNGSNQRP	262
SEQ ID NO:6	-----PMGHMG-----FWGDTILVN	LTPNPMYDVER-KIYRFRLNGSNAP	261
Consensus		** * : : * * : . 28	
	370 380 390 400 410 420		
SEQ ID NO:2	NLSLDN-G--GEFIQIGSDGGLPRSVKLNSFSI	APAEERFDILIDFAAFE-GQSIILANS	319
SEQ ID NO:16	NLSLDN-G--GEFIQIGSDGGLPRSVMLNSFSI	APAEERFDILIDFAAFE-GQSIILANS	319
SEQ ID NO:18	ILKFSNP--LSFWQIGNDGGFLPAPVQLSOLL	MSPAERADVIVDFSQTFPGTEIILENT	380
SEQ ID NO:20	PLELDG---HSLHQIAQDGIARFSPETDSVFL	TPGNRADVLVRGG-QP-GTYYLKQQA	317
SEQ ID NO:26	LLALAG---HTLHQIAADGNPYDEVVPRDO	ILLPPSERVEVLVQASTQL-GSYEFRTL	227
SEQ ID NO:14	EFRLSD-G--GEFTQIASDRGLLPAPYTTTT	LPLSPAERADIVDFSRYFVGSVVLENA	319
SEQ ID NO:6	RLALLRGNQRMRFVVLGVGGLLDTPKEVNE	ILVAPGERIDILVDFRDASVNDVIKLYN	321
Consensus	: : : * : . : . * : * : : : .		41
	430 440 450 460 470 480		
SEQ ID NO:2	-----EGCGG-----DVPNET	DANIMQFRVTK-PLAQKDES	351
SEQ ID NO:16	-----EGCGG-----DVPNET	DANIMQFRVTK-PLAQKDES	351
SEQ ID NO:18	GP-----DEPFGGGE	PDSDFSADATTRQVMQFRV--PLTTADT	422
SEQ ID NO:20	-----YDQ-----GRGEVP	EIIATVVVGPPSFMRLPWLL	348
SEQ ID NO:26	-----WGD-----DFQAE	PDVVLATMVVAG---EAITPAPL	255
SEQ ID NO:14	-----YFPEPS	SNKEILRFDVVR---SAYDPSSV	344
SEQ ID NO:6	PHNLIGMGMIGMRMGMERGMGMNGMNM	DGMADNSEFEVMEFRVTK--DSAYDKSIP	379
Consensus		: : * .	43
	490 500 510 520 530 540		
SEQ ID NO:2	PKYLASYPSVRHERIQNLRLTKLAG--TQDQY	G---RPVLL--LNN-----KRWHDPVT	398
SEQ ID NO:16	PKYLASYPSVQHERIQNLRLTKLAG--TQDQY	G---RPVLL--LNN-----KRWHDPVT	398
SEQ ID NO:18	PNLLELPAITGLGAATNRQVSLNEEDSAVL	FGVGPRALLGTLDSERGEPEIRGWDAIT	482
SEQ ID NO:20	PTPAL-HRTITDEEVTSRSIVFSV--QPAPAG	---EMFPRFLIDG-----HTFSPDRVD	397
SEQ ID NO:26	PTALIPYEDLRDVPVDNIRVTTFEE--PGAP	-----L--YLAIDG-----KHFDPRVD	300
SEQ ID NO:14	PARLATLPPTAAPTQTRNYTLDFDVQTGAGS	-----IS-----G-----KTWDEQRVD	387
SEQ ID NO:6	QRLSEVTPINTDGAQVQRITLGMRRMVFTIN	-----GETWEDGYANP-----QDINNPKVL	430
Consensus		: : : .	45
	550 560 570 580 590 600		
SEQ ID NO:2	EAPKAGSTEIWSIINPT-RGTHPIHL	LVLSFRVLDRRPFDTARFEERGELAYTGPAVPPP	457
SEQ ID NO:16	EAPKAGSTEIWSIINPT-RGTHPIHL	LVLSFRVLDRRPFDTARFEERGELAYTGPAVPPP	457
SEQ ID NO:18	ENPALGSIEVWEIHNT-EDAHPIHIEVAF	EVVNRQPFEGS---ARG-----PE	528
SEQ ID NO:20	HSIPLCSVEEWTVINNH-REDHPFHIEVNA	FEVTHLNGDRLP-----	438
SEQ ID NO:26	QTVKLGAEEWIVRNTS-SEWHPFHIEVND	FOVIANNNEAVN-----	341
SEQ ID NO:14	TTVRQGDTEVWEIKNTHPFIPHNEHIE	LVDFRILDIDGKPPT-----PG	431
SEQ ID NO:6	EEQNNGDVVIEYVNT-GMYHPMTHGFO	FOVLERSLGPLR-----	471
Consensus	* * * : * : : : .		54
	610 620 630 640 650 660		
SEQ ID NO:2	PSEKGWKDTVQSHAGEVLRIAVTFGP-YTG	--RYVWHCHILEHEDYDMRPM	514
SEQ ID NO:16	PSEKGWKDTVQSHAGEVLRIAVTFGP-YTG	--RYVWHCHILEHEDYDMRPM	514
SEQ ID NO:18	VWEGGFKDTVIAYPEEITRVKAHFD--LPG	--LYVWHCHIVEHEDNEMRPY-FIGP	580
SEQ ID NO:20	--RPRWHDVINVPFGTATFTRTFED-FTG	--KFVLHCHLLVHEDLGMOTVEVT	488
SEQ ID NO:26	--THGYEDSVALPPHSETTMRMKFLD-FSG	--KFVYHCHILGHEDFGMAVVEVVE	392
SEQ ID NO:14	--DAGLKDTVRIQGETARILVHFDFPYSG	--RYYYHCHLIDHSSMGANLEITR	483
SEQ ID NO:6	ATDLGWKDTVIVARMETVRIVDM	SHPYNEHQIYLLHCHILEHDEGVMVNYRVNA	527
Consensus	* : : : : * : * : .		66

FIGURE 12

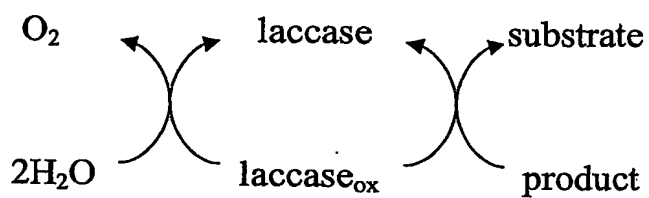


Figure 12B

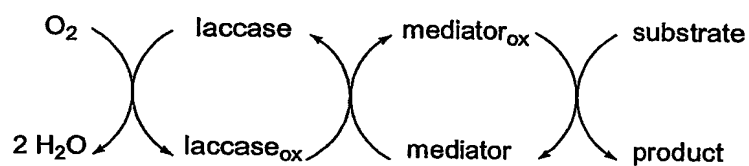


Figure 12C

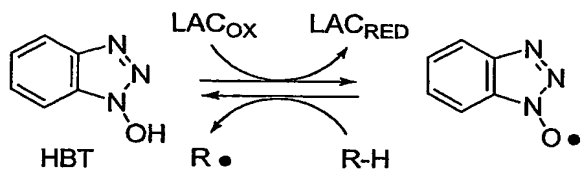


Figure 12D

